

An amino acid sequence of human, type I, IMPDH protein

IMPDH = INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1
, 514 residues

MADYLISGGT GYVPEDGLTA QQLFASADDL TYNDFLILPG FIDFIADEVD LTSALTRKIT LKTPLISSPM DTVTEADMAI AMALMGGIGF IHHNCTPEFQ ANEVRKVKNF EQGFITDPVV LSPSHTVGDV LEAKMRHGFS GIPITETGTM GSKLVGIVTS RDIDFLAEKD HTTLLSEVMT PRIELVVAPA GVTLKEANEI LQRSKKGKLP IVNDCDELVA IIARTDLKKN RDYPLASKDS QKQLLCGAAV GTREDDKYRL DLLTQAGVDV IVLDSSQGNS VYQIAMVHYI KQKYPHLQVI GGNVVTAAQA KNLIDAGVDG LRVGMGCGSI CITQEVMACG RPQGTAVYKV AEYARRFGVP IIADGGIQTV GHVVKALALG ASTVMMGSLL AATTEAPGEY FFSDGVRLKK YRGMGSLDAM EKSSSSQKRY FSEGDKVKIA QGVSGSIQDK GSIQKFVPYL IAGIQHGCQD IGARSLSVLR SMMYSGELKF EKRTMSAQIE GGVHGLHSYE KRLY

An amino acid sequence of human, type II IMPDH protein

IMPDH = INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2
, 514 residues

The underlined region correlates with the subdomain region

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD
LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ
ANEVRKVKKY EQGFITDPVV LSPKDRVRDV FEAKARHGFC GIPITDTGRM
GSRLVGIISS RDIDFLKEEE HDCFLEEIMT KREDLVVAPA GITLKEANEI
LQRSKKGKLP IVNEDDELVA IIARTDLKKN RDYPLASKDA KKQLLCGAAI
GTHEDDKYRL DLLAQAGVDV VVLDSSQGNS IFQINMIKYI KDKYPNLQVI
GGNVVTAAQA KNLIDAGVDA LRVGMGSGSI CITQEVLACG RPQATAVYKV
SEYARRFGVP VIADGGIQNV GHIAKALALG ASTVMMGSLL AATTEAPGEY
FFSDGIRLKK YRGMGSLDAM DKHLSSQNRY FSEADKIKVA QGVSGAVQDK
GSIHKFVPYL IAGIQHSCQD IGAKSLTQVR AMMYSGELKF EKRTSSAQVE

# FIGURE 3

and The Subdomain of Wild-Type, Human, IMPDH is Replaced with an Oligo-Peptide

Phe-514		
10 Leu-243	oligo	peptide
Met-1 Tyr-110		



The amino acid sequence of the modified IMPDH-DKT polypeptide 384 residues.

The substitute tri-peptide DKT sequence is highlighted in bold print

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD
LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ
ANEVRKVKKY **DKT**LLCGAAI GTHEDDKYRL DLLAQAGVDV VVLDSSQGNS
IFQINMIKYI KDKYPNLQVI GGNVVTAAQA KNLIDAGVDA LRVGMGSGSI
CITQEVLACG RPQATAVYKV SEYARRFGVP VIADGGIQNV GHIAKALALG
ASTVMMGSLL AATTEAPGEY FFSDGIRLKK YRGMGSLDAM DKHLSSQNRY
FSEADKIKVA QGVSGAVQDK GSIHKFVPYL IAGIQHSCQD IGAKSLTQVR
AMMYSGELKF EKRTSSAQVE GGVHSLHSYE KRLF





The nucleotide sequence of type II, IMPDH-DKT cDNA

 $\verb|atggccgactacctgattagtggggcacgtcctacgtgccagacggactcacagcacagcacgctct| \\$ teaactgeggagacggecteacctacaatgactttctcattctccctgggtacatcgacttcactgcaga ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttcctctcccatg gacacagtcacagaggctgggatggccatagcaatggcgcttacaggcggtattggcttcatccaccaca actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatatgacaagaccctgctgtgtgg ggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctggtgtggatgta gtggttttggactcttcccagggaaattccatcttccagatcaatatgatcaagtacatcaaagacaaat accctaatctcoaagtcattggaggcaatgtggtcactgctgcccaggccaagaacctcattgatgcagg tgtggatgccctgcgggtgggcatgggaagtggctccatctgcattacgcaggaagtgctggcctgtggg cggccccaagcaacagcagtgtacaaggtgtcagagtatgcacggcgctttggtgttccggtcattgctg atggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcatgatggg ctctctcctggctgccaccactgaggcccctggtgaatacttcttttccgatgggatccggctaaagaaa tatcgcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagtgaag ctgacaaaatcaaagtggcccagggagtgtctggtgctgtgcaggacaaagggtcaatccacaaatttgt cccttacctgattgctggcatccaacactcatgccaggacattggtgccaagagcttgacccaagtccga gccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccaggtggaaggtggcgtcc atagcctccattcgtatgagaagcggcttttctga



The amino acid sequence of the modified IMPDH-SPS polypeptide 384 residues.

The substitute tri-peptide SPT sequence is highlighted in bold print.

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD
LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ
ANEVRKVKKY SPSLLCGAAI GTHEDDKYRL DLLAQAGVDV VVLDSSQGNS
IFQINMIKYI KDKYPNLQVI GGNVVTAAQA KNLIDAGVDA LRVGMGSGSI
CITQEVLACG RPQATAVYKV SEYARRFGVP VIADGGIQNV GHIAKALALG
ASTVMMGSLL AATTEAPGEY FFSDGIRLKK YRGMGSLDAM DKHLSSQNRY
FSEADKIKVA QGVSGAVQDK GSIHKFVPYL IAGIQHSCQD IGAKSLTQVR
AMMYSGELKF EKRTSSAQVE GGVHSLHSYE KRLF



#### FIGURE 7

The nucleotide sequence of type II, IMPDH-SPS cDNA

 ${\tt atggccgactacctgattagtgggggcacgtcctacgtgccagacggactcacagcacagcacgctct}$ tcaactgcggagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcactgcaga ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttcctctcccatg gacacagtcacagaggctgggatggccatagcaatggcgcttacaggcggtattggcttcatccaccaca actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatattctccgagcctgctgtgtgg ggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctggtgtggatgta gtggttttggactcttcccagggaaattccatcttccagatcaatatgatcaagtacatcaaagacaaat accetaatetecaagteattggaggeaatgtggteactgetgeceaggeeaagaaceteattgatgeagg tgtggatgccctgcgggtgggcatgggaagtggctccatctgcattacgcaggaagtgctggcctgtggg cggccccaagcaacagcagtgtacaaggtgtcagagtatgcacggcgctttggtgttccggtcattgctg atggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcatgatggg ctctctcctggctgccaccactgaggcccctggtgaatacttcttttccgatgggatccggctaaagaaa tatcgcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagtgaag ctgacaaaatcaaagtggcccagggagtgtctggtgctgtgcaggacaaagggtcaatccacaaatttgt cccttacctgattgctggcatccaacactcatgccaggacattggtgccaagagcttgacccaagtccga gccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccaggtggaaggtggcgtcc atagcctccattcgtatgagaagcggcttttctga



The amino acid sequence of the type II, modified  ${\tt IMPDH\text{-}GSG}$  polypeptide

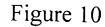
The substitute tri-peptide GSG sequence is highlighted in bold print

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ ANEVRKVKKY **GSG**LLCGAAI GTHEDDKYRL DLLAQAGVDV VVLDSSQGNS IFQINMIKYI KDKYPNLQVI GGNVVTAAQA KNLIDAGVDA LRVGMGSGSI CITQEVLACG RPQATAVYKV SEYARRFGVP VIADGGIQNV GHIAKALALG ASTVMMGSLL AATTEAPGEY FFSDGIRLKK YRGMGSLDAM DKHLSSQNRY FSEADKIKVA QGVSGAVQDK GSIHKFVPYL IAGIQHSCQD IGAKSLTQVR AMMYSGELKF EKRTSSAQVE GGVHSLHSYE KRLF



The nucleotide sequence of type II, IMPDH-GSG cDNA

atggccgactacctgattagtgggggcacgtcctacgtgccagacgacggactcacagcacagcacgtct  ${\tt tcaactgcggagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcactgcaga}$  $\verb|ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttcctctcccatg|$ gacacagtcacagaggctgggatggccatagcaatggcgcttacaggcggtattggcttcatccaccaca  $\verb|actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatatggttccggcctgctgtgtgg|$ ggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctggtgtggatgta gtggttttggactcttcccagggaaattccatcttccagatcaatatgatcaagtacatcaaagacaaat accctaatctccaagtcattggaggcaatgtggtcactgctgcccaggccaagaacctcattgatgcagg tgtggatgccctgcgggtgggcatgggaagtggctccatctgcattacgcaggaagtgctggcctgtggg cggccccaagcaacagcagtgtacaaggtgtcagagtatgcacggcgctttggtgttccggtcattgctg atggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcatgatggg ctctctcctggctgccaccactgaggcccctggtgaatacttcttttccgatgggatccggctaaagaaa tatcgcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagtgaag ctgacaaaatcaaagtggcccagggagtgtctggtgctgtgcaggacaaagggtcaatccacaaatttgt  $\verb|cccttacctgattgctggcatccaacactcatgccaggacattggtgccaagagcttgacccaagtccga|\\$ gccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccaggtggaaggtggcgtcc atagcctccattcgtatgagaagcggcttttctga



The amino acid sequence of the modified IMPDH-SPT polypeptide 384 residues.

The substitute tri-peptide SPT sequence is highlighted in bold print.

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ ANEVRKVKKY SPTLLCGAAI GTHEDDKYRL DLLAQAGVDV VVLDSSQGNS IFQINMIKYI KDKYPNLQVI GGNVVTAAQA KNLIDAGVDA LRVGMGSGSI CITQEVLACG RPQATAVYKV SEYARRFGVP VIADGGIQNV GHIAKALALG ASTVMMGSLL AATTEAPGEY FFSDGIRLKK YRGMGSLDAM DKHLSSQNRY FSEADKIKVA QGVSGAVQDK GSIHKFVPYL IAGIQHSCQD IGAKSLTQVR AMMYSGELKF EKRTSSAQVE GGVHSLHSYE KRLF





The nucleotide sequence of type II, IMPDH-SPT cDNA

atggccgactacctgattagtgggggcacgtcctacgtgccagacgacggactcacagcacagcagctct ${\tt tcaactgcggagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcactgcaga}$ ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttcctctcccatg gacacagtcacagaggctgggatggccatagcaatggcgcttacaggcggtattggcttcatccaccaca actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatattctccgactctgctgtgtgg ggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctggtgtggatgta gtggttttggactcttcccagggaaattccatcttccagatcaatatgatcaagtacatcaaagacaaat accctaatctccaagtcattggaggcaatgtggtcactgctgcccaggccaagaacctcattgatgcagg tgtggatgccetgcgggtgggcatgggaagtggctccatctgcattacgcaggaagtgctggcctgtggg cggccccaagcaacagcagtgtacaaggtgtcagagtatgcacggcgctttggtgttccqgtcattgctg atggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcatgatggg ctctctcctggctgccaccactgaggcccctggtgaatacttcttttccgatgggatccggctaaagaaa tatcgcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagtgaag ctgacaaaatcaaagtggcccagggagtgtctggtgctgtgcaggacaaagggtcaatccacaaatttgt cccttacctgattgctggcatccaacactcatgccaggacattggtgccaagagcttgacccaagtccga atagcctccattcgtatgagaagcggcttttctga



The nucleotide sequence of type II, IMPDH-SPTQ cDNA

atggccgactacctgattagtgggggcacgtcctacgtgccagacgacggactcacagcacagcactct tcaactgcggagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcactgcaga ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttcctctcccatg gacacagteacagaggetgggatggecatageaatggegettacaggeggtattggetteatecaceaca actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatattctccgactcagctgctgtg tggggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctggtgtggat gtagtggttttggactcttcccagggaaattccatcttccagatcaatatgatcaagtacatcaaagaca aataccctaatctccaagtcattggaggcaatgtggtcactgctgcccaggccaagaacctcattgatgc aggtgtggatgccctgcgggtgggcatgggaagtggctccatctgcattacgcaggaagtgctggcctgt gggcggccccaagcaacagcagtgtacaaggtgtcagagtatgcacggcgctttggtgttccggtcattg ctgatggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcatgat gggctctctctcctggctgccaccactgaggcccctggtgaatacttcttttccgatgggatccggctaaag aaatatcgcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagtg aagctgacaaaatcaaagtggcccagggagtgtctggtgctgtgcaggacaaagggtcaatccacaaatt tgtcccttacctgattgctggcatccaacactcatgccaggacattggtgccaagagcttgacccaagtc cgagccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccaggtggaaggtggcg tccatagcctccattcgtatgagaagcggcttttctga

The amino acid sequence of the modified type II, IMPDH-AGRP polypeptide 385 residues

The substitute tetra-peptide AGRP sequence is highlighted in bold print.

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD
LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ
ANEVRKVKKY AGRPLLCGAA IGTHEDDKYR LDLLAQAGVD VVVLDSSQGN
SIFQINMIKY IKDKYPNLQV IGGNVVTAAQ AKNLIDAGVD ALRVGMGSGS
ICITQEVLAC GRPQATAVYK VSEYARRFGV PVIADGGIQN VGHIAKALAL
GASTVMMGSL LAATTEAPGE YFFSDGIRLK KYRGMGSLDA MDKHLSSQNR
YFSEADKIKV AQGVSGAVQD KGSIHKFVPY LIAGIQHSCQ DIGAKSLTQV
RAMMYSGELK FEKRTSSAQV EGGVHSLHSY EKRLF





The nucleotide sequence of type II, IMPDH-AGRP

atggccgactacctgattagtgggggcacgtcctacgtgccagacgacggactcacagcacagcacct tcaactgcggagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcactgcaga ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttcctctcccatg gacacagtcacagaggctgggatggccatagcaatggcgcttacaggcggtattggcttcatccaccaca actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatatgctggtcgtccgctgctgtg tggggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctggtgtggat gtagtggttttggactcttcccagggaaattccatcttccagatcaatatgatcaagtacatcaaagaca aataccctaatctccaagtcattggaggcaatgtggtcactgctgcccaggccaagaacctcattgatgc aggtgtggatgccctgcgggtgggcatgggaagtggctccatctgcattacgcaggaagtgctggcctgt gggcggccccaagcaacagcagtgtacaaggtgtcagagtatgcacggcgctttggtgttccggtcattg ctgatggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcatgat gggctctctccctggctgccaccactgaggcccctggtgaatacttcttttccgatgggatccggctaaag aaatatcgcggtatgggttetetegatgccatggacaagcacetcagcagccagaacagatatttcagtg aagctgacaaaatcaaagtggcccagggagtgtctggtgctgtgcaggacaaagggtcaatccacaaatt tgtcccttacctgattgctggcatccaacactcatgccaggacattggtgccaagagcttgacccaagtc cgagccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccaggtggaaggtggcg tccatagcctccattcgtatgagaagcggcttttctga



The amino acid sequence of type II, modified IMPDH-NSPL polypeptide

The substitute tri-peptide is highlighted in bold print

MADYLISGGT SYVPDDGLTA QQLFNCGDGL TYNDFLILPG YIDFTADQVD LTSALTKKIT LKTPLVSSPM DTVTEAGMAI AMALTGGIGF IHHNCTPEFQ ANEVRKVKKY NSPLLLCGAA IGTHEDDKYR LDLLAQAGVD VVVLDSSQGN SIFQINMIKY IKDKYPNLQV IGGNVVTAAQ AKNLIDAGVD ALRVGMGSGS ICITQEVLAC GRPQATAVYK VSEYARRFGV PVIADGGIQN VGHIAKALAL GASTVMMGSL LAATTEAPGE YFFSDGIRLK KYRGMGSLDA MDKHLSSQNR YFSEADKIKV AQGVSGAVQD KGSIHKFVPY LIAGIQHSCQ DIGAKSLTQV RAMMYSGELK FEKRTSSAQV EGGVHSLHSY EKRLF



The nucleotide sequence of type II, IMPDH-NSPL cDNA

atggccgactacctgattagtgggggcacgtcctacgtgccagacggactgacagcacagcagctcttcaactgcggagacggcctcacctacaatgactttctcattctccctgggtacatcgacttcactgcaga ccaggtggacctgacttctgctctgaccaagaaaatcactcttaagaccccactggtttcctctcccatg gacacagteacagaggetgggatggccatagcaatggegettacaggeggtattggettcatecaccaca actgtacacctgaattccaggccaatgaagttcggaaagtgaagaaatataactctccgcttctgctgtg tggggcagccattggcactcatgaggatgacaagtataggctggacttgctcgcccaggctggtgtggat gtagtggttttggactcttcccagggaaattccatcttccagatcaatatgatcaagtacatcaaagaca aataccctaatctccaagtcattggaggcaatgtggtcactgctgcccaggccaagaacctcattgatgc aggtgtggatgccctgcgggtgggcatgggaagtggctccatctgcattacgcaggaagtgctggcctgt gggcggccccaagcaacagcagtgtacaaggtgtcagagtatgcacggcgctttggtgttccggtcattg ctgatggaggaatccaaaatgtgggtcatattgcgaaagccttggcccttggggcctccacagtcatgat gggctctctcctggctgccaccactgaggcccctggtgaatacttcttttccgatgggatccggctaaag aaatatcgcggtatgggttctctcgatgccatggacaagcacctcagcagccagaacagatatttcagtg aagctgacaaaatcaaagtggcccagggagtgtctggtgctgtgcaggacaaagggtcaatccacaaatt tgtcccttacctgattgctggcatccaacactcatgccaggacattggtgccaagagcttgacccaagtc cgagccatgatgtactctggggagcttaagtttgagaagagaacgtcctcagcccaggtggaaggtggcg tecatageetecattegtatgagaageggettttetga

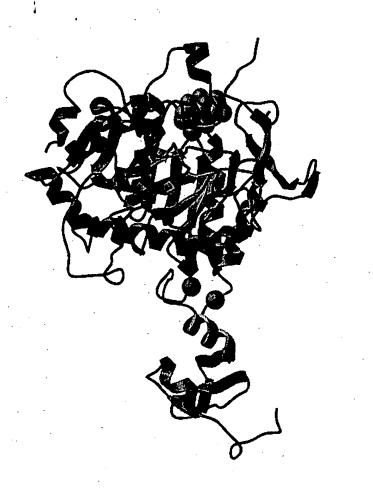


The amino acid sequence of the type I modified IMPDH-DKT polypeptide

The substitute tri-peptide DKT is highlighted in bold print

MADYLISGGT GYVPEDGLTA QQLFASADGL TYNDFLILPG FIDFIADEVD LTSALTRKIT LKTPLISSPM DTVTEADMAI AMALMGGIGF IHHNCTPEFQ ANEVRKVKKF DKTLLCGAAV GTREDDKYRL DLLTQAGVDU IVLDSSQGNS VYQIAMVHYI KQKYPHLQVI GGNVVTAAQA KNLIDAGVDG LRVGMGCGSI CITQEVMACG RPQGTAVYKV AEYARRFGVP IIADGGIQTV GHVVKALALG ASTVMMGSLL AATTEAPGEY FFSDGVRLKK YRGMGSLDAM EKSSSQKRY FSEGDKVKIA QGVSGSIQDK GSIQKFVPYL IAGIQHGCQD IGARSLSVLR SMMYSGELKF EKRTMSAQIE GGVHGLHSYE KRLY

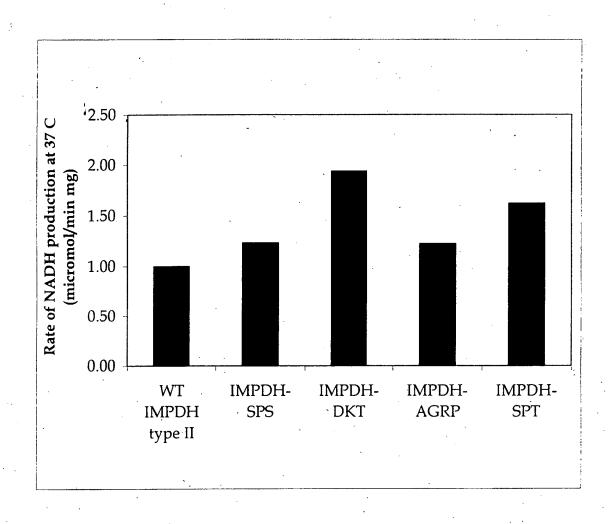
A schematic representation of the distance that the substitute oligo-peptides are designed to span in a folded modified IMPDH polypeptide.



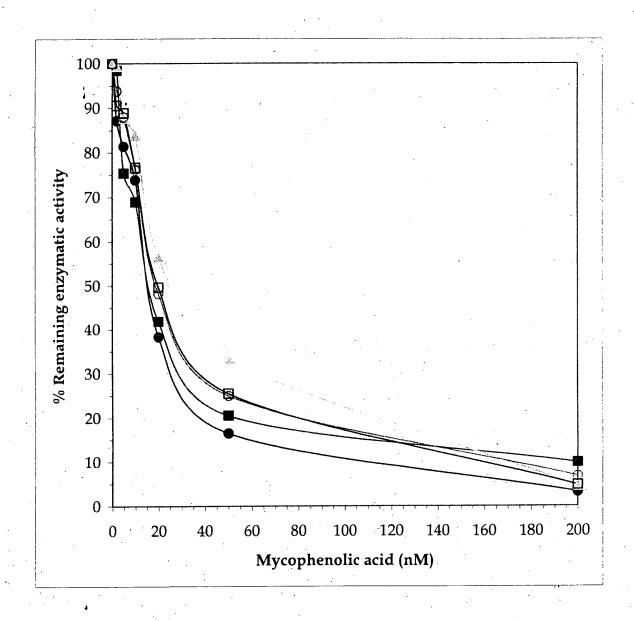
CATALYTIC CORE DOMAIN

SUBDOMAIN

The Rate of NADH Production at 37  $^{\circ}\text{C}$  for Wild-Type IMPDH (type II) and Various Modified IMPDH Multimers.



MPA Inhibits the Activity of Various Modified IMPDH Polypeptides.

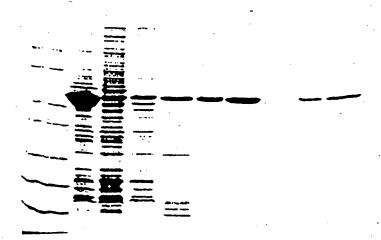


- wild-type, type II IMPDH
- O type II, IMPDH-AGRP
- type II, IMPDH-SPS
- type II, IMPDH-SPT
- ▲ type II, IMPDH-DKT

E DEICOL

#### FIGURE 21

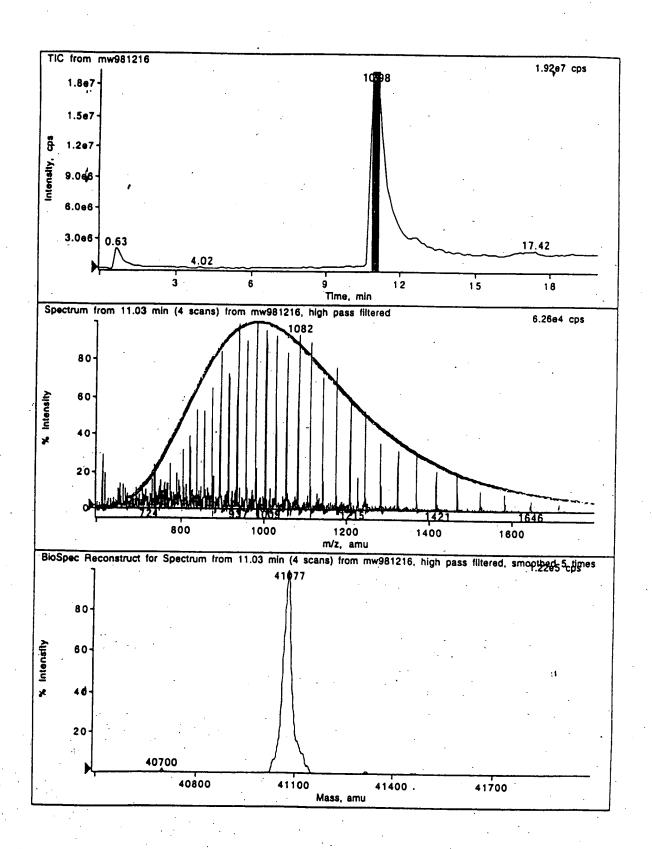
1 2 3 4 5 6 7 8 9 10



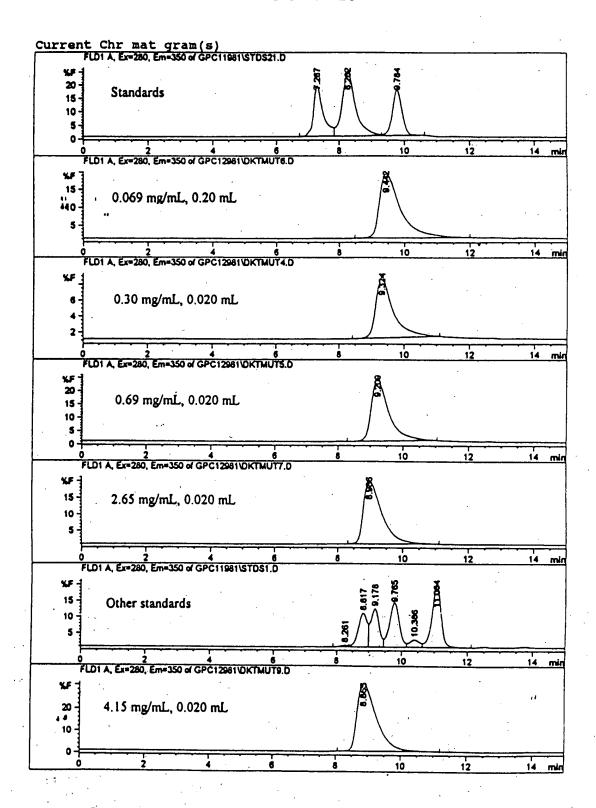
Lane #

- 1: Novex standards (25 µL)
- 2: Total cell lysate (1 µL, 12 µg; before ultracentrifugation)
- 3: Soluble lysate (2.5 μL, 10 μg; after 100,000 x g, 1 hr, 4 °C)
- 4: Unbound AE sample (13 μL, ~10 μg)
- 5: Blue dye column, frs. #32-70 (25 μL, 4.5 μg)
- 6: IMP affinity column, IMP eluted (10  $\mu$ L, ~1.5  $\mu$ g)
- 7: IMP affinity column, IMP eluted (20 µL, ~3.0 µg)
- 8: Unbound protein to IMP column (25  $\mu$ L, ~2.0  $\mu$ g)
- 9: IMP affinity column (from AE fr. #1-10,  $10 \mu L$ ,  $1.2 \mu g$ )
- 10: IMP affinity column (from AE fr. #1-10, 25 μL, 3.0 μg)

## FIGURE 22



#### FIGURE 23





The nucleotide sequence of type I, IMPDH-DKT

 $\verb|atggcggactacctgatcagcggcggcaccggctacgtgcccgaggatgggctcaccgcgcagcagctct|$ tcgccagcgccgacggcctcacctacaacgacttcctgattctcccaggattcatagacttcatagctga tgaggtggacctgacctgacccggaagatcacgctgaagacgccactgatctcctcccccatg actgcaccccagagttccaggccaacgaggtgcggaaggtcaagaagtttgacaaaaccctgctctgtgg atagtettggaetegteceaagggaatteggtgtateaaategeeatggtgeattacateaaacagaagt tgtggacgggctgcgcttgcgttccatctgcatcacccaggaagtgatggcctgtggt cggccccagggcactgctgtgtacaaggtggctgagtatgcccggcgctttggtgtgcccatcatagccg atggcggcatccagaccgtgggacacgtggtcaaggccctggcccttggagcctccacagtgatgatggg ctccctgctggccgccactacggaggcccctggcgagtacttcttctcagacggggtgcggctcaagaag taccggggcatgggctcactggatgccatggagaagcagcagcagcagcagaaacgatacttcagcgagg gecetaceteatageaggeatecaacaggetgecaggatateggggecegeageetgtetgteettegg tccatgatgtactcaggagagctcaagtttgagaagcggaccatgtcggcccagattgagggtggtgtcc atggcctgcactcttacgaaaagcggctgtactga